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OM protein - protein search, using sw model

Run on: June 3, 2003, 15:05:33 ; Search time 15 Seconds
(without alignments)
468.805 Million cell updates/sec

Title: US-09-887-784-4

Perfect score: 1274

Sequence: 1 AVSKGEELFTGVVPILVELD.....VILGFVTAAGITLGMDELYK 239

Scoring table: BloSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 100%

Database : Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA;*
1: /cgn2_6/pidata/1/1aa/5A_COMB_pep;*
2: /cgn2_6/pidata/1/1aa/5B_COMB_pep;*
3: /cgn2_6/pidata/1/1aa/6A_COMB_pep;*
4: /cgn2_6/pidata/1/1aa/6B_COMB_pep;*
5: /cgn2_6/pidata/1/1aa/pCTMS_COMB_pep;*
6: /cgn2_6/pidata/1/1aa/backfile1.pep;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB ID	Description
1	1263	99.1	239	4	US-09-172-063-3	Sequence 3, AppI
2	1263	99.1	239	4	US-09-513-783A-46	Sequence 4, AppI
3	1263	99.1	239	4	US-09-516-919-4	Sequence 1, AppI
4	1263	99.1	281	4	US-09-062-102-1	Sequence 1, AppI
5	1263	99.1	281	4	US-09-364-946-1	Sequence 2, AppI
6	1263	99.1	294	4	US-09-513-783A-2	Sequence 2, AppI
7	1263	99.1	323	4	US-09-172-003-21	Sequence 21, AppI
8	1263	99.1	364	4	US-09-513-783A-170	Sequence 6, AppI
9	1263	99.1	459	2	US-08-518-253-2	Sequence 170, APP
10	1263	99.1	642	2	US-08-518-253-2	Sequence 2, AppI
11	1263	99.1	642	4	US-08-818-232-6	Sequence 6, AppI
12	1263	99.1	642	4	US-08-818-232-6	Sequence 2, AppI
13	1263	99.1	642	4	US-08-513-783A-172	Sequence 6, AppI
14	1263	99.1	652	2	US-08-818-233-4	Sequence 4, AppI
15	1263	99.1	652	4	US-08-818-251-4	Sequence 4, AppI
16	1263	99.1	783	4	US-09-513-783A-176	Sequence 176, APP
17	1263	99.1	805	4	US-09-513-783A-178	Sequence 178, APP
18	1263	99.1	890	4	US-09-513-783A-174	Sequence 174, APP
19	1263	99.1	941	4	US-09-513-783A-172	Sequence 172, APP
20	1263	99.1	1407	4	US-08-514-559A-628	Sequence 628, APP
21	1260	98.9	239	4	US-09-098-339-4	Sequence 4, AppI
22	1259	98.8	239	4	US-09-121-531-14	Sequence 14, AppI
23	1254	98.4	239	4	US-09-513-783A-48	Sequence 48, AppI
24	1254	98.4	1056	4	US-09-513-783A-32	Sequence 32, AppI
25	1254	98.4	1610	4	US-09-513-783A-22	Sequence 22, AppI
26	1249	98.0	247	3	US-08-893-327-18	Sequence 18, AppI
27	1248	98.0	238	3	US-08-893-327-16	Sequence 16, AppI

ALIGNMENTS

RESULT 1
US-09-172-063-3
; Sequence 3, Application US/09172063
; Patent No. 6150176
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; APPLICANT: Illopis, Juan
; APPLICANT: Wachtel, Rebekka M.
; APPLICANT: Remington, S. James
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR A BIOLOGICAL SAMPLE
; FILE REFERENCE: 07257/071001
; CURRENT APPLICATION NUMBER: US/09/172,063
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 09/094,359
; EARLIER FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 239
TYPE: PRT
ORGANISM: Aequorea victoria
FEATURE: VARIANT
NAME/KEY: (0)-(0)
LOCATION: (0)-(0)
OTHER INFORMATION: EGFP
US-09-172-063-3

Qy 1 AVSKGEELFTGVVPILVELDGVNGHKFYSVGPILVYDGVNGHKFYSVGEGEQDATYQLTKFICIGKLKPWPT 60
Db 1 AVSKGEELFTGVVPILVYDGVNGHKFYSVGEGEQDATYQLTKFICIGKLKPWPT 60
Qy 2 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 2 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 3 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 3 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 4 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 4 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 5 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 5 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 6 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 6 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 7 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 7 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 8 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 8 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 9 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 9 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 10 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 10 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 11 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 11 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 12 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 12 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 13 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 13 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 14 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 14 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 15 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 15 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 16 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 16 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 17 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 17 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 18 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 18 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 19 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 19 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 20 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 20 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 21 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 21 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 22 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 22 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 23 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 23 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 24 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 24 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 25 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 25 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 26 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 26 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Qy 27 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120
Db 27 LYTTLTYGVQCFSRYPDHMKDFKFFKSAMPSSYQVQERTIFFRDGNYKTRAEVKFGDTL 120

RESULT 2
US-09-513-783A-46
; Sequence 46, Application US/09513783A
; Patent No. 641659
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening

; FILE REFERENCE: 97-022-L1
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46

; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EGFP

US-09-513-783A-46

Query Match 99.1%; Score 1263; DB 4; Length 239;
Best Local Similarity 99.2%; Pred. No. 1.2e-12;
Matches 237; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVSKEELTGVPILVLDGVNGHKSVSGESEGDDATYGRKLKPCTGKLPFWPT 60

Db 1 MVSKEELTGVPILVLDGVNGHKSVSGESEGDDATYGRKLKPCTGKLPFWPT 60

Qy 61 LVTTLTYGQCFSRPDAMKQHDFEFSAMPEGVQERTIFFRDGNYKTRAEVKFESDTL 120

Db 61 LVTTLTYGQCFSRPDAMKQHDFEFSAMPEGVQERTIFFRDGNYKTRAEVKFESDTL 120

Qy 121 VNRIELKGIDFEKGINTLGHKLEYNNSHNVTIMADQKNGIKVNFKIRHNIEDGSVOLA 180

Db 121 VNRIELKGIDFEKGINTLGHKLEYNNSHNVTIMADQKNGIKVNFKIRHNIEDGSVOLA 180

Qy 181 DHYQQNTPIGDGPVLLPDHYLSTSALSKDPNEKRDMVLLGFTTAAGITLGMDELYK 239

Db 181 DHYQQNTPIGDGPVLLPDHYLSTSALSKDPNEKRDMVLLGFTTAAGITLGMDELYK 239

RESULT 3
US-09-316-919-4
; Sequence 4, Application US/09316919
; Patent No. 6469154
; GENERAL INFORMATION:
; APPLICANT: Baird, Geoffrey Y.
; TITLE OF INVENTION: FLUORESCENT PROTEIN INDICATORS
; FILE REFERENCE: 07257/073001
; CURRENT APPLICATION NUMBER: US/09/316,919
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Aequarea victoria

US-09-316-919-4

Query Match 99.1%; Score 1263; DB 4; Length 239;
Best Local Similarity 99.2%; Pred. No. 1.2e-12;
Matches 237; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVSKEELTGVPILVLDGVNGHKSVSGESEGDDATYGRKLKPCTGKLPFWPT 60

Db 1 MVSKEELTGVPILVLDGVNGHKSVSGESEGDDATYGRKLKPCTGKLPFWPT 60

Qy 61 LVTTLTYGQCFSRPDAMKQHDFEFSAMPEGVQERTIFFRDGNYKTRAEVKFESDTL 120

Db 61 LVTTLTYGQCFSRPDAMKQHDFEFSAMPEGVQERTIFFRDGNYKTRAEVKFESDTL 120

Qy 121 VNRIELKGIDFEKGINTLGHKLEYNNSHNVTIMADQKNGIKVNFKIRHNIEDGSVOLA 180

Db 121 VNRIELKGIDFEKGINTLGHKLEYNNSHNVTIMADQKNGIKVNFKIRHNIEDGSVOLA 180

Qy 181 DHYQQNTPIGDGPVLLPDHYLSTSALSKDPNEKRDMVLLGFTTAAGITLGMDELYK 239

Db 181 DHYQQNTPIGDGPVLLPDHYLSTSALSKDPNEKRDMVLLGFTTAAGITLGMDELYK 239

RESULT 4
US-09-062-102-1
; Sequence 1, Application US/09062102
; Patent No. 6130313
; GENERAL INFORMATION:
; APPLICANT: Kain, Steve
; APPLICANT: Li, Xiangling
; TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
; FILE REFERENCE: D6100
; CURRENT APPLICATION NUMBER: US/09/062,102
; CURRENT FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: US 60/060,855
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of the EGFP-MODC4 22-461 fusion protein.
; Patent No. 6130313
; SEQ ID NO 1
; LENGTH: 281

Query Match 99.1%; Score 1263; DB 4; Length 281;
Best Local Similarity 99.2%; Pred. No. 1.6e-127;
Matches 237; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVSKEELTGVPILVLDGVNGHKSVSGESEGDDATYGRKLKPCTGKLPFWPT 60

Db 1 MVSKEELTGVPILVLDGVNGHKSVSGESEGDDATYGRKLKPCTGKLPFWPT 60

Qy 61 LVTTLTYGQCFSRPDAMKQHDFEFSAMPEGVQERTIFFRDGNYKTRAEVKFESDTL 120

Db 61 LVTTLTYGQCFSRPDAMKQHDFEFSAMPEGVQERTIFFRDGNYKTRAEVKFESDTL 120

Qy 121 VNRIELKGIDFEKGINTLGHKLEYNNSHNVTIMADQKNGIKVNFKIRHNIEDGSVOLA 180

Db 121 VNRIELKGIDFEKGINTLGHKLEYNNSHNVTIMADQKNGIKVNFKIRHNIEDGSVOLA 180

Qy 181 DHYQQNTPIGDGPVLLPDHYLSTSALSKDPNEKRDMVLLGFTTAAGITLGMDELYK 239

Db 181 DHYQQNTPIGDGPVLLPDHYLSTSALSKDPNEKRDMVLLGFTTAAGITLGMDELYK 239

RESULT 5
US-09-364-946-1
; Sequence 1, Application US/09364946
; Patent No. 6306600
; GENERAL INFORMATION:
; APPLICANT: Kain, Steve
; APPLICANT: Li, Xiangling
; TITLE OF INVENTION: Rapidly Degrading GFP-Fusion Proteins and Methods
; FILE REFERENCE: D6100CP/D2
; CURRENT APPLICATION NUMBER: US/09/364,946
; CURRENT FILING DATE: 1999-07-30
; EARLIER APPLICATION NUMBER: US 09/191,233
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: artificial sequence

US-09-364-946-1

Query Match 99.1%; Score 1263; DB 4; Length 281;
Best Local Similarity 99.2%; Pred. No. 1.2e-12;
Matches 237; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVSKEELTGVPILVLDGVNGHKSVSGESEGDDATYGRKLKPCTGKLPFWPT 60

Db 1 MVSKEELTGVPILVLDGVNGHKSVSGESEGDDATYGRKLKPCTGKLPFWPT 60

Qy 61 LVTTLTYGQCFSRPDAMKQHDFEFSAMPEGVQERTIFFRDGNYKTRAEVKFESDTL 120

Db 61 LVTTLTYGQCFSRPDAMKQHDFEFSAMPEGVQERTIFFRDGNYKTRAEVKFESDTL 120

FEATURE: OTHER INFORMATION: Sequence of the EGFP-MDC422-461 fusion protein.
; Patent No. 6305600
US-09-364-946-1

Query Match Score 99.1%; Pred. No. 1.6e-127; Length 281;
Best Local Similarity 99.2%; Pred. No. 1.6e-127;
Matches 237; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Query Match Score 99.1%; Pred. No. 1.6e-127; Length 281;
Best Local Similarity 99.2%; Pred. No. 1.6e-127;
Matches 237; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVSKGEELFTGVPIVILVEDGNGKFSVSGEGDATYKLTKFICITGKLKPVPNPT 60
Db 1 MVSKGEELFTGVPIVILVEDGNGKFSVSGEGDATYKLTKFICITGKLKPVPNPT 60
Qy 61 LVTTLISYGQCFCSRYPDKMKQHDEFFKSAMPEGYQERTIFFKDDQNYKTRAEVKEFGDTL 120
Db 61 LVTTLISYGQCFCSRYPDKMKQHDEFFKSAMPEGYQERTIFFKDDQNYKTRAEVKEFGDTL 120
Qy 121 VNRIELKGIDFKEGDNILGHKLEYNNSHNYTMADKQKNGIKVNFKIRHNIEDGSVOLA 180
Db 121 VNRIELKGIDFKEGDNILGHKLEYNNSHNYTMADKQKNGIKVNFKIRHNIEDGSVOLA 180
Qy 181 DHYQONTPIGDGPVLLPDNHYLSTOSALSKDNEKRDHMVLGFTAAGITLGMDELYK 239
Db 181 DHYQONTPIGDGPVLLPDNHYLSTOSALSKDNEKRDHMVLGFTAAGITLGMDELYK 239
Db 181 DHYQONTPIGDGPVLLPDNHYLSTOSALSKDNEKRDHMVLGFTAAGITLGMDELYK 239

RESULT 6
US-09-513-783A-2

; Sequence 2, Application US/09513783A

; Patent No. 6416939
; GENERAL INFORMATION:
; APPLICANT: Giuriano, Kenneth A.
; INVENTOR: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-11
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence:
; OTHER INFORMATION: GFP-DEVD Annexin II construct
US-09-513-783A-2

Query Match Score 99.1%; Pred. No. 1.7e-127; Length 294;
Best Local Similarity 99.2%; Pred. No. 1.7e-127;
Matches 237; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Query Match Score 99.1%; Pred. No. 1.7e-127; Length 294;
Best Local Similarity 99.2%; Pred. No. 1.7e-127;
Matches 237; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVSKGEELFTGVPIVILVEDGNGKFSVSGEGDATYKLTKFICITGKLKPVPNPT 60
Db 1 MVSKGEELFTGVPIVILVEDGNGKFSVSGEGDATYKLTKFICITGKLKPVPNPT 60
Qy 61 LVTTLISYGQCFCSRYPDKMKQHDEFFKSAMPEGYQERTIFFKDDQNYKTRAEVKEFGDTL 120
Db 61 LVTTLISYGQCFCSRYPDKMKQHDEFFKSAMPEGYQERTIFFKDDQNYKTRAEVKEFGDTL 120
Qy 121 VNRIELKGIDFKEGDNILGHKLEYNNSHNYTMADKQKNGIKVNFKIRHNIEDGSVOLA 180
Db 121 VNRIELKGIDFKEGDNILGHKLEYNNSHNYTMADKQKNGIKVNFKIRHNIEDGSVOLA 180
Qy 181 DHYQONTPIGDGPVLLPDNHYLSTOSALSKDNEKRDHMVLGFTAAGITLGMDELYK 239
Db 181 DHYQONTPIGDGPVLLPDNHYLSTOSALSKDNEKRDHMVLGFTAAGITLGMDELYK 239
Db 181 DHYQONTPIGDGPVLLPDNHYLSTOSALSKDNEKRDHMVLGFTAAGITLGMDELYK 239

RESULT 8

US-09-085-305-6
; Sequence 6, Application US/09085305

; Patent No. 6191269
; GENERAL INFORMATION:
; APPLICANT: Pollock, Allan
; INVENTOR: Lovett, David H.
; TITLE OF INVENTION: Selective Induction of Apoptosis in Malignant Cancer Cells by Delivery of N-Terminal Interleukin-1 Alpha Pro-Peptide
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,305
; FILING DATE: 29-MAY-1998
; Sequence 21, Application US/09172063
; Patent No. 6150176

CLASSIFICATION:
 PROR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Francis, Carol L.
 REGISTRATION NUMBER: 36,513
 REFERENCE/DOCKET NUMBER: 6510/1020US1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-327-3400
 TELEX: 650-327-3231
 INVENTORY FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 364 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-085-305-6

Query Match 99.1% Score 1263; DB 4; Length 364;
 Best Local Similarity 99.2%; Pred. No. 2, 3e-127;
 Matches 237; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVSGEELFTGVVPLVLDGDNHFKFSVSGEGDATYGRKLTKFICHTGKLFVLPWPPT 60
 Db 126 MVSGEELFTGVVPLVLDGDNHFKFSVSGEGDATYGRKLTKFICHTGKLFVLPWPPT 185

Qy 61 LVTTLSYGVOCFSRYPDMKQHDFKSAMPBYYQERTIFFPRDDGAKYKTRAEVKEFDTL 120
 Db 186 LVTTLSYGVOCFSRYPDMKQHDFKSAMPBYYQERTIFFKDDGNYKTRAEVKEFDTL 245

Qy 121 VNRBLKGDFKEDGNLIGHKLEYNTNSHNYIMADRKQNGIKVNFKIRINIEDGSVOLA 180
 Db 246 VNRBLKGDFKEDGNLIGHKLEYNTNSHNYIMADRKQNGIKVNFKIRINIEDGSVOLA 305

Qy 181 DHYQONTPIGDGPVLLPDNHYLSTSALSQSKDNEKRDHMVLGLFTTAAGITLGMDLYK 239
 Db 306 DHYQONTPIGDGPVLLPDNHYLSTSALSQSKDNEKRDHMVLLEFTTAAGITLGMDLYK 364

RESULT 9
 US-09-513-783A-170
 Patent No. 6416559
 GENERAL INFORMATION:
 APPLICANT: Kapoor, Ravi A.
 TITLE OF INVENTION: A System for Cell Based Screening
 FILE REFERENCE: 97-022-LI
 CURRENT APPLICATION NUMBER: US/09/513,783A
 CURRENT FILING DATE: 2000-02-25
 NUMBER OF SEQ ID NOS: 190
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 170
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: GFP-HSP27

Query Match 99.1% Score 1263; DB 4; Length 459;
 Best Local Similarity 99.2%; Pred. No. 3, 3e-127;
 Matches 237; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVSGEELFTGVVPLVLDGDNHFKFSVSGEGDATYGRKLTKFICHTGKLFVLPWPPT 60
 Db 1 MVSGEELFTGVVPLVLDGDNHFKFSVSGEGDATYGRKLTKFICHTGKLFVLPWPPT 60

Qy 61 LVTTLSYGVOCFSRYPDMKQHDFKSAMPBYYQERTIFFPRDDGAKYKTRAEVKEFDTL 120
 Db 464 LVTTLSYGVOCFSRYPDMKQHDFKSAMPBYYQERTIFFKDDGNYKTRAEVKEFDTL 523

Qy 1 MVSGEELFTGVVPLVLDGDNHFKFSVSGEGDATYGRKLTKFICHTGKLFVLPWPPT 60
 Db 404 MVSGEELFTGVVPLVLDGDNHFKFSVSGEGDATYGRKLTKFICHTGKLFVLPWPPT 60

Qy 61 LVTTLSYGVOCFSRYPDMKQHDFKSAMPBYYQERTIFFPRDDGAKYKTRAEVKEFDTL 120
 Db 524 LVTTLSYGVOCFSRYPDMKQHDFKSAMPBYYQERTIFFKDDGNYKTRAEVKEFDTL 523

Qy 121 VNRBLKGDFKEDGNLIGHKLEYNTNSHNYIMADRKQNGIKVNFKIRINIEDGSVOLA 180
 Db 524 VNRBLKGDFKEDGNLIGHKLEYNTNSHNYIMADRKQNGIKVNFKIRINIEDGSVOLA 583

Qy 181 DHYQONTPIGDGPVLLPDNHYLSTSALSQSKDNEKRDHMVLGLFTTAAGITLGMDLYK 239
 Db 584 DHYQONTPIGDGPVLLPDNHYLSTSALSQSKDNEKRDHMVLLEFTTAAGITLGMDLYK 642

RESULT 11

US-08-818-253-6
; Sequence 6 , Application US/08818253
; Patent No. 5998.04

GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR DETECTION OF ANALYTES

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASESEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/818,253
FILING DATE: 14-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hille, Ph.D.; Lisa A.
REGISTRATION NUMBER: 38 A.
REFERENCE/DOCKET NUMBER: 07257/043001
REFERENCE/DOCKET NUMBER: 07257/043001

INFORMATION FOUNDATION.
TELEPHONE: 619/678-5010
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 642 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

FRAGMENT TYPE:		Internal	
QY	Db	QY	Db
Query Match	99.1%	Score 1263; DB 2;	Length 642;
Best Local Similarity	99.2%	Pred. No. 5	4e-17;
Matches	237;	Mismatches	1;
		Indels	
QY	1	MSKGEBELFTGVPIVLLGVDYNGHKFSESGEGDATYGRKLTFICIT	
QY	404	MSKGEBELFTGVPIVLLGVDYNGHKFSESGEGDATYGRKLTFICIT	
QY	61	LVTTLGVQCESRTSPDHAKRQHDFFKSAMPPEGYQERIIFKDGDGYKTR	
QY	464	LVTTLGVQCSRTSPDHAKRQHDFFKSAMPPEGYQERIIFKDGDGYKTR	
Db	121	VRIELAKIDFKEDGNILGKLETNYNSINIVIMADRKNGIKVNFKIRAH	
Db	524	VRIELKGIDSKEDGNILGKLETNYNSINIVIMADSKNGIKVNFKIRIN	
QY	181	DHQQTNPQGCPVLLPDNHVLSTPOSALSKDPEKRDWMLGQFTAAIGT	
QY			

RESULT 12
US-08-818-252-2
; Sequence 2, Application US/08818252B
; Patent No. 6197936
; GENERAL INFORMATION:

```

; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/04/2001
; CURRENT APPLICATION NUMBER: US/09/818,252B
; CURRENT FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Aequorea victoria
US-08-818-252-2

Query Match Score 1263; Db 4; Length 642;
Best Local Similarity 99.2%; Pred. No. 5.4e-127;
Matches 237; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY          1 MVSKEELFTGIVVPLVLEDGYDYNQGHKFVSGESEGEGDATYQKLTKFICTTGKLPVPVPT 60
Db          404 MVSKEELFTGIVVPLVLEDGYDYNQGHKFVSGESEGEGDATYQKLTKFICTTGKLPVPVPT 463
        61 LVTTSYGTQCFSSXPDHMKQHDFFPSAMPEYYQERTTIFKDDGNYKTAEVKFEGDL 120
Db          464 LVTTSYGTQCFSSXPDHMKQHDFFPSAMPEYYQERTTIFKDDGNYKTAEVKFEGDL 523
        121 VNRTELKGTDKEGDNILGHKLEYNNSHNYTIMADQKQNGIKVNFKIRHNIEFGSYOLA 180
Db          524 VNRTELKGTDKEGDNILGHKLEYNNSHNYTIMADQKQNGIKVNFKIRHNIEFGSYOLA 583
        181 DHYQONTPIGDGPVLLPDNHYLSTSQALSKDOPNEKDHAVLLGFTAAAGITLGMDELYK 239
Db          584 DHYQONTPIGDGPVLLPDNHYLSTSQALSKDOPNEKDHAVLLGFTAAAGITLGMDELYK 642

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RESULT 13
US-08-818-252-6
Sequence 6, Application US/08818752B
Patent No. 617998
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SE
TITLE OF INVENTION: DETECTION OF ANALYTE
FILE REFERENCE: 07257/042001
CURRENT APPLICATION NUMBER: US/08/818, 252B
CURRENT FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Past-SEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 64:2
TYPE: PRT
ORGANISM: Aequorea victoria

US-08-818-252-6
Qy 1 MYSKGEELETFGPVPLVLLDGYNGKFKTSV
Query Match
Best Local Similarity 99.18; Score 1263;
Matches 237; Conservative 1; Mismatch
Db 404 MYSKGEELETFGPVPLVLLDGYNGKFKTSV
Qy 61 LYTFLSYGVQCTPSRYPDHMKHDDFFKSAMP

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Db	464	LVTLYTGQCFSRPDHMKDFFKAMPESYQERTIFFKDGNYKTRAEVKFEGDTL	52
Qy	121	VNFIELKGIDFEDGNLGHKEYNTASHNVTMADQKNGIKVNFKIRHNIEGDSVLA	18
Db	524	VNFIELKGIDFEDGNLGHKEYNTASHNVTMADQKNGIKVNFKIRHNIEGDSVLA	58
Qy	181	DHQONTPIGDGVLLDNNYLSTQSALSQSKPNEKRDHNVLLFGTTAAGITLGADELYK	239

Db 584 DHYQONTPIGDGPVLLPDNHYLSTSALSQSKDPNEKRDMVYLLEFTAAAGITLGMDELYK 642

RESULT 14
US-08-818-253-4
Sequence 4, Application US/08818253
Patent No. 599804

GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR DETECTION OF ANALITES

NUMBER OF SEQ ID NOS: 56
CURRENT APPLICATION NUMBER: US/08/818,252B
CURRENT FILING DATE: 1997-03-14
SEQ ID NO 4
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 652
TYPE: PRT
ORGANISM: Aequorea victoria
US-08-818-253-4

Query Match 99.1%; Score 1263; DB 4; Length 652;
Best Local Similarity 99.2%; Pred. No. 5.5e-127;
Matches 237; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVSKEELFTGVQCSRPDHMKQHDFKSAMPEGYQERTIFPKDDGNYKTRAEVKFEGDTL 60
Db 404 MVSKEELFTGVQCSRPDHMKQHDFKSAMPEGYQERTIFPKDDGNYKTRAEVKFEGDTL 463

QY 61 LVTTLSYGVQCSRPDHMKQHDFKSAMPEGYQERTIFPKDDGNYKTRAEVKFEGDTL 120
Db 464 LVTTLTYGVQCSRPDHMKQHDFKSAMPEGYQERTIFPKDDGNYKTRAEVKFEGDTL 523

QY 121 VNRIELKGIDFEDGNILGHKLEYNNSHNVYIMADKQNGKIKVNFKIRINIIEDSVQLA 180
Db 524 VNRIELKGIDFEDGNILGHKLEYNNSHNVYIMADKQNGKIKVNFKIRINIIEDSVQLA 583

QY 181 DHYQONTPIGDGPVLLPDNHYLSTSALSQSKDPNEKRDMVYLLEFTAAAGITLGMDELYK 239
Db 584 DHYQONTPIGDGPVLLPDNHYLSTSALSQSKDPNEKRDMVYLLEFTAAAGITLGMDELYK 642

Search completed: June 3, 2003, 15:09:32
Job time : 26 secs

RESULT 15
US-08-818-252-4
Sequence 4, Application US/08818252B
Patent No. 6197928
GENERAL INFORMATION:

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-818-253-4

Query Match 99.1%; Score 1263; DB 2; Length 652;
Best Local Similarity 99.2%; Pred. No. 5.5e-127;
Matches 237; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVSKEELFTGVQCSRPDHMKQHDFKSAMPEGYQERTIFPKDDGNYKTRAEVKFEGDTL 60
Db 404 MVSKEELFTGVQCSRPDHMKQHDFKSAMPEGYQERTIFPKDDGNYKTRAEVKFEGDTL 463

QY 61 LVTTLSYGVQCSRPDHMKQHDFKSAMPEGYQERTIFPKDDGNYKTRAEVKFEGDTL 120
Db 464 LVTTLTYGVQCSRPDHMKQHDFKSAMPEGYQERTIFPKDDGNYKTRAEVKFEGDTL 523

QY 121 VNRIELKGIDFEDGNILGHKLEYNNSHNVYIMADKQNGKIKVNFKIRINIIEDSVQLA 180
Db 524 VNRIELKGIDFEDGNILGHKLEYNNSHNVYIMADKQNGKIKVNFKIRINIIEDSVQLA 583

QY 181 DHYQONTPIGDGPVLLPDNHYLSTSALSQSKDPNEKRDMVYLLEFTAAAGITLGMDELYK 239
Db 584 DHYQONTPIGDGPVLLPDNHYLSTSALSQSKDPNEKRDMVYLLEFTAAAGITLGMDELYK 642